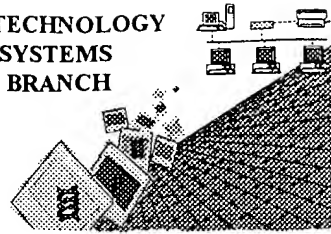


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/105,117 J
Source: 1600
Date Processed by STIC: 12/13/2002

1653
RECEIVED

JAN 02 2003

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



1600

RAW SEQUENCE LISTING

DATE: 12/13/2002

PATENT APPLICATION: US/09/105,117J

TIME: 15:15:03

Input Set : A:\Seq_listing_US_korrigiert141102.txt

Output Set: N:\CRF4\12132002\I105117J.raw

3 <110> APPLICANT: Forschungszentrum Juelich GmbH
 5 <120> TITLE OF INVENTION: Process for the microbial production of amino acids by
 6 boosted activity of export carriers
 8 <130> FILE REFERENCE: 1
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/105,117J
 11 <141> CURRENT FILING DATE: 1998-06-17
 13 <160> NUMBER OF SEQ ID NOS: 5
 15 <170> SOFTWARE: PatentIn Ver. 2.0

*See following
pages for explanation*

ERRORED SEQUENCES

E--> 208 <210> SEQ ID NO: (complement to <210> 1)

209 <221> NAME/KEY: unsure

210 <222> LOCATION: CDS (2)..(652)

211 <223> OTHER INFORMATION: orf3

W--> 212 <220> FEATURE:

213 <221> NAME/KEY: gene

214 <222> LOCATION: CDS (1421)..(2293)

215 <223> OTHER INFORMATION: LysG

W--> 217 <400> 3

218 a gat act cct ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg 49

219 Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala

220 1 5 10 15

222 tct gga aag gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctg 97

223 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu

224 20 25 30

226 aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg 145

227 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu

228 35 40 45

230 att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg 193

231 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro

232 50 55 60

234 ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt 241

235 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu

236 65 70 75 80

238 ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctg acg gac aaa 289

239 Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys

240 85 90 95

242 tat ctg gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc 337

243 Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser

244 100 105 110

246 ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag 385

**Does Not Comply
Corrected Diskette Needed**

09/105,1175 2

SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH

<120> Process for the microbial production of amino acids by
boosted activity of export carriers

<130> 1

<140> US/09/105,117 PCT/DE96/02485

<141> 1998-06-17

<150>

<151>

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 2374

<212> DNA

<213> Corynebacterium glutamicum

<220> (Lyse)

<221> gene

<222> CDS (1016)..(1726)

<223>

<400> 1

ccatttgctg aaggtgttac tctgcctggc ccaattcctg cgggcgaaga agtgaaaaac 60
cctgaacctt ttcagaagta actaaggccg caatccctcg attgctgcat caacgacggc 120
gtctgtgagt ctagctagag atctagattc caggcgccat cgttgccaat acatcggtgt 180
gtcaatgggt atctcatcga ggaggatcac ttctcctgct tttagcatgg gagcagcttg 240
ggtttcggga agaagtcccc aaccaaggcc tcggcgaatt gcttcaccaa aaccttcgcg 300
cgacgggaca atggatacgc gctgcgccc cacaggacca tcgacgcgcc cgtccaggtc 360
acgggtcttga agcacatctt tgggaccgaa gcgtaagacg ggcacgcag cccaatctag 420
tttcccatca accatgtagg catcccgcaa tgaggggggt gcaatggcca agtggcgcat 480
ggttccaagt tctactactt cacatccgcg caggggatta gttcacggg ttaccgctcc 540
taaaacatct ccacgccgca gcaaggataa tgtgtgcgct tcatcttcca agcgcagcgt 600
gagcgttgct ccacccaag aagctacctc gttgaacacg ggaggaaacc atgtggatag 660
cgaatctgcy ttgatggcga tggttaacgg gatttcagca aggcgtccag atagttgcgc 720
tttagtttct gcttgacgca acaccatttt ccgcgtgct tgcacaagga cttcaccgcg 780
ttcggttgct ttggccggtt ggggtgcgca taccaacact cgaccacgt gatgctcgag 840
agctttaacg cgctgactca ccgccgaggg ggaatggaa agggctaagg aggcgccttc 900
gaagctgcct tcatcaatga ttgagagcaa agtgtccagt tgaatggggt tcatgaagct 960

This is a prior application, and
needs to go on <150> line.

Please insert prior application
filing date on <151>

<220> never has a response. It is a "header"
only. Insert
any explanatory
material on
<223> line.

09/109/11753

atattaaacc atgttaagaa ccaatcattt tacttaagta cttccatagg tcacg atg 1018
Met
1

gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt ctt 1066
Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu
5 10 15

tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga att 1114
Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile
20 25 30

aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac 1162
Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp
35 40 45

gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc aat 1210
Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn
50 55 60 65

gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct tac 1258
Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr
70 75 80

ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag 1306
Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys
85 90 95

gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat 1354
Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp
100 105 110

gac acg cct ttg ggc ggt tgc gcg gtg gcc act gac acg cgc aac cgg 1402
Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg
115 120 125

gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc 1450
Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro
130 135 140 145

atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg 1498
Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu
150 155 160

gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac acc 1546
Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr
165 170 175

gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc tgg 1594
Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp
180 185 190

ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg tcc 1642
Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser
195 200 205

09/105,1175. 4

agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg atg 1690
 Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met
 210 215 220 225

acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag ttttcgcggg 1736
 Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
 230 235

ttttggaatc ggtggccttc gcccaaagt tgatgccggc gtcgtgggaa atctcatcga 1796

tcgcctccaa ctggcggtca gaaaactcca agttgttgag tgaatcaagg ctgttgcca 1856

gctgctcaac tgacgaagca ccaatcaatg cactggtcac ggtatccgag ccgtactctc 1916

cttgctcgag cagcaccat gcaagcgcca tctgcgcaag tgactgccg cgttcctggg 1976

cgatgtcatt gagcttgagg accatatcaa tattgttcac gttcaacatg ccctcagaca 2036

gggacttacc ctggctggcg cgggaacct ctggaattcc atcgagatat ttgtccgtga 2096

gcaggccctg cgcaagtggg gagaaagcaa tgacgccaag accattgttg gcagctgact 2156

gcaacaagtt ctaccgtca tcgccgggt cctccacca acgattaatg atggaatagc 2216

ttggctgatg aatcagaagc gggcagccct cctccgcat gaactcagcc gcctccgctg 2276

tgagctctgg accgtaggaa gaaataccca cgtaaagagc cttccagac gcaacaatgt 2336

cacgcaatgc gtacatggtt tcttccaaag gattatct 2374

<210> 2

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<220> (LysE)

2237

<400> 2

Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
 1 5 10 15

Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
 20 25 30

Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
 35 40 45

Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
 50 55 60

Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
 65 70 75 80

Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
 85 90 95

09/105,1175⁵

Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
 100 105 110
 Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn
 115 120 125
 Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
 130 135 140
 Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
 145 150 155 160
 Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
 165 170 175
 Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
 180 185 190
 Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
 195 200 205
 Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val
 210 215 220
 Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
 225 230 235

<210> 3
 <211> 2374
 <212> DNA
 <213> Corynebacterium glutamicum
 <220> (complement to <210> 1)
 <221> unsure
 <222> CDS (2)..(652)
 <223> orf3
 <220>
 <221> gene
 <222> CDS (1421)..(2293)
 <223> LysG

(complement to SEQ ID NO 1) please use this format
 instead of <210> 1; otherwise,
 the CRF software
 interprets
 <210> 1 as a
new
sequence

<400> 3
 a gat act cct ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg 49
 Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
 1 5 10 15
 tct gga aag gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc 97
 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
 20 25 30
 aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg 145
 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
 35 40 45

09/105/11756

att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg	193
Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro	
50 55 60	
ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt	241
Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu	
65 70 75 80	
ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa	289
Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys	
85 90 95	
tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc	337
Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser	
100 105 110	
ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag	385
Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys	
115 120 125	
ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg	433
Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala	
130 135 140	
ctt gca tgg gtg ctg cgc gag caa gga gag tac gcc gcg gat acc gtg	481
Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val	
145 150 155 160	
acc agt gca ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc	529
Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser	
165 170 175	
ctt gat tca ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg	577
Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala	
180 185 190	
atc gat gag att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc	625
Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala	
195 200 205	
acc gat tcc aaa acc cgc gaa aac taa cccatcaaca tcagtttgat	672
Thr Asp Ser Lys Thr Arg Glu Asn	
210 215	
ggccaatgcg gtcattcacia ctgccacgac gacgttgatc cagcgccaca ccttggggct	732
ggacagcggg cgtgacaatg ctgctgcgcc gaaaccacc agcgggaacc agatcaggct	792
tgccgcgaac gcgccagcgg cgaaaatcca ccgtccggtg tcgccgtatt gcgcgccgac	852
gccgccgata aacacaaacg cgtccaaata cgcattcggg ttcaaccagg tcagcacgat	912
tgccatcaac atgggcttta cccaaaccg ctgcttatcg acgctcacct ccaccgcac	972
ccggttgccg gtgtcagtgg ccaccgccga accgccaaa ggcgtgtcat cgggcacggt	1032

09/105,1125 ?

tggttctgtt tcttcaatga tctgtggcgc ttccaccttg tttgtcatgg cgtctttcgc	1092
tgccatgacg gcaaaccata acaggtaagc gatgccaccc cagcgcataa tatcgagcac	1152
gatcggcgcg gcattggaca aaagatcaac gcccaagggtg ccggcgatga acaaaaagac	1212
gtcagaaatt aaacacacga gaagaaccgc aatgagtcct tcgcgcttaa ttccttgttt	1272
aatcaccagt acattctgcg gtccgatgga cagtaaaaga ctggccccca aaagcagacc	1332
tgtaatgaag atttccatga tcaccatcgt gacctatgga agtacttaag taaaatgatt	1392
ggttcttaac atggtttaat atagcttc atg aac ccc att caa ctg gac act	1444
Met Asn Pro Ile Gln Leu Asp Thr	
220 225	
ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc tcc tta gcc	1492
Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala Ser Leu Ala	
230 235 240	
ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa gct ctc gag	1540
Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys Ala Leu Glu	
245 250 255	
cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg gcc aaa gca	1588
His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro Ala Lys Ala	
260 265 270	
acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa atg gtg ttg	1636
Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys Met Val Leu	
275 280 285	
ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt gct gaa atc	1684
Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu Ala Glu Ile	
290 295 300 305	
ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca tgg ttt cct	1732
Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr Trp Phe Pro	
310 315 320	
ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg ctc acg ctg	1780
Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr Leu Thr Leu	
325 330 335	
cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg cgt gga gat	1828
Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg Arg Gly Asp	
340 345 350	
gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg gga tgt gaa	1876
Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala Gly Cys Glu	
355 360 365	
gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca acc ccc tca	1924
Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala Thr Pro Ser	
370 375 380 385	
ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg gct gcg atg	1972

09/105,1175

8

Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met
 390 395 400
 ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac cgt gac ctg 2020
 Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp Arg Asp Leu
 405 410 415
 gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta tcc att gtc 2068
 Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val Ser Ile Val
 420 425 430
 ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc ctt ggt tgg 2116
 Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly Leu Gly Trp
 435 440 445
 gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa gca gga gaa 2164
 Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys Ala Gly Glu
 450 455 460 465
 gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg tat tgg caa 2212
 Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met Tyr Trp Gln
 470 475 480
 cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca gac gcc gtc 2260
 Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr Asp Ala Val
 485 490 495
 gtt gat gca gca atc gag gga ttg cgg cct tag ttacttctga aaaggttcag 2313
 Val Asp Ala Ala Ile Glu Gly Leu Arg Pro
 500 505
 gggtttttcac ttcttcgccc gcaggaattg ggccaggcag agtaacacct tcagcaaattg 2373
 g 2374

<210> 4
 <211> 216
 <212> PRT
 <213> Corynebacterium glutamicum
 <220> (orf3)
 <223> 4
 <400> 4

Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
 1 5 10 15
 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
 20 25 30
 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
 35 40 45
 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
 50 55 60
 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
 65 70 75 80

09/105,1175 9

Gly	Val	Ile	Ala	Phe	Ser	Pro	Leu	Ala	Gln	Gly	Leu	Leu	Thr	Asp	Lys
				85					90					95	
Tyr	Leu	Asp	Gly	Ile	Pro	Glu	Gly	Ser	Arg	Ala	Ser	Gln	Gly	Lys	Ser
			100					105					110		
Leu	Ser	Glu	Gly	Met	Leu	Asn	Val	Asn	Asn	Ile	Asp	Met	Val	Arg	Lys
		115					120					125			
Leu	Asn	Asp	Ile	Ala	Gln	Glu	Arg	Gly	Gln	Ser	Leu	Ala	Gln	Met	Ala
	130					135					140				
Leu	Ala	Trp	Val	Leu	Arg	Glu	Gln	Gly	Glu	Tyr	Gly	Ala	Asp	Thr	Val
145					150					155					160
Thr	Ser	Ala	Leu	Ile	Gly	Ala	Ser	Ser	Val	Glu	Gln	Leu	Asp	Asn	Ser
			165						170					175	
Leu	Asp	Ser	Leu	Asn	Asn	Leu	Glu	Phe	Ser	Asp	Ala	Glu	Leu	Glu	Ala
			180					185					190		
Ile	Asp	Glu	Ile	Ser	His	Asp	Ala	Gly	Ile	Asn	Ile	Trp	Ala	Lys	Ala
	195					200						205			
Thr	Asp	Ser	Lys	Thr	Arg	Glu	Asn								
210						215									

<210> 5
 <211> 290
 <212> PRT
 <213> Corynebacterium glutamicum
 <220> (LysG)
 <223> 5
 <400> 5

Met	Asn	Pro	Ile	Gln	Leu	Asp	Thr	Leu	Leu	Ser	Ile	Ile	Asp	Glu	Gly
1				5					10					15	
Ser	Phe	Glu	Gly	Ala	Ser	Leu	Ala	Leu	Ser	Ile	Ser	Pro	Ser	Ala	Val
			20					25					30		
Ser	Gln	Arg	Val	Lys	Ala	Leu	Glu	His	His	Val	Gly	Arg	Val	Leu	Val
		35					40					45			
Ser	Arg	Thr	Gln	Pro	Ala	Lys	Ala	Thr	Glu	Ala	Gly	Glu	Val	Leu	Val
	50					55					60				
Gln	Ala	Ala	Arg	Lys	Met	Val	Leu	Leu	Gln	Ala	Glu	Thr	Lys	Ala	Gln
65					70				75						80
Leu	Ser	Gly	Arg	Leu	Ala	Glu	Ile	Pro	Leu	Thr	Ile	Ala	Ile	Asn	Ala
				85					90					95	
Asp	Ser	Leu	Ser	Thr	Trp	Phe	Pro	Pro	Val	Phe	Asn	Glu	Val	Ala	Ser
		100						105					110		

09/105,1175 10

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
165 170 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu
210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala
225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser
260 265 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu
275 280 285

Arg Pro
290

FZJ 9910 PCT/US 8/8 12.11.02
US 09/105,117

delete